

REPLACEMENT SHEET

FIG. 13

| ROW | PRIMER SEQUENCE | SEQ ID NO | SEQUENCED SEQUENCE | SEQ ID NO | PREDICTED GAM RNA | SEQ ID NO | DIST-ANCE | GAM-NAME |
|-----|-----------------|-----------|--------------------|-----------|--|---------------------|-----------|---------------------------|
| 1* | AATTGCTTGAAC | 4204948 | CCAGGAAGTGG | 4204977 | AATTGCTTGAACCCAGGAAGTGG | 4205006 | 0 | 25-A |
| 2* | ACTGCACTCC | 4204949 | AGCCTGGGC | 4204978 | ACTGCACTCCAGCCTGGGCTAC | 4205007 | 0 | 351661-A |
| 3 | CACTGCACTC | 4204950 | CAGCCCAGCAACA | 4204979 | CACTGCACTCCAGCCCAGCAA | 4205008 | 0 | 351946-A |
| 4 | CTAGACTGAAG | 4204951 | CTCCTTGAGGAC | 4204980 | CTAGACTGAAGCTCCTTGAGGA | 4205009 | 0 | 352759-A |
| 5 | GAAGTTTGAAG | 4204952 | CCTGTTGTTCA | 4204981 | GAAGTTTGAAGCCTGTTGTTCA | 4205010 | 0 | 4426-A |
| 6 | TCACTGCAAC | 4204953 | CTCCACCA | 4204982 | (TCACTGCAACCTCCACCACGTG), (TCACTGCAACCTCCACCACGCCT) | 4205011, 4205094 | 0 | (357950-A), (352721-A) |
| 7* | TCTAAAGAGAAAG | 4204954 | GAAGTTCAGA | 4204983 | TCTAAAGAGAAAGGAAGTTCAGA | 4205012 | 0 | 337950-A |
| 8 | GGGCAGTGG | 4204955 | GCTGGAA | 4204984 | GGGCAGTGGAGCTGGAATGATGT | 4205013 | 1 | 351996-A |
| 9 | AATTGCTTGAAC | 4204956 | CCAAGAAGTGG | 4204985 | AATCACTTGAACCCAAGAAGTG | 4205014 | 2 | 351874-A |
| 10 | AGCAGCCC | 4204957 | GGGTTTTGT | 4204986 | AGCAAGACCAGGGTTTGTT | 4205015 | 2 | 352083-A |
| 11 | AGGCAAGACG | 4204958 | GACCAGA | 4204987 | AGGCAGAGAGGACCAGAGACT | 4205016 | 2 | 351944-A |
| 12 | AGGGAAAGAAT | 4204959 | TAATGTGAA | 4204988 | GGGAAATAATTAATGTGAAGTC | 4205017 | 2 | 353325-A |
| 13 | AGGGAAAGAAT | 4204960 | TAATGTGAG | 4204989 | AGGAAAAAAATTAATGTGAGTC | 4205018 | 2 | 352649-A |
| 14 | ATTCAGTTG | 4204961 | CCCATGTT | 4204990 | (ATTCATTGCCATGTTG), (TATTGATGCCATGGTGA) | 4205095, 4205019 | 2 | A),(352957-A,352960-A) |
| 15 | CTAGACTGAAG | 4204962 | CTCCTTGAGG | 4204991 | CTGGACTGAGCTCCTTGAGGCC | 4205020 | 2 | 352288-A |
| 16 | TTCAGAGTGGT | 4204963 | TAAGTTCTG | 4204992 | TTCTGATGGTTAAGTTCTGTCA | 4205021 | 2 | 353875-A |
| 17 | TTCAGAGTGGT | 4204964 | TAAGTTCTGC | 4204993 | TTCAAGTGTAAAGTTCTGCTT | 4205022 | 2 | 351940-A |
| 18 | AGCAGCCC | 4204965 | GAAGGAAGC | 4204994 | AGGCCAAGAAGGAAGCAGAGG | 4205023 | 3 | 352496-A |
| 19 | AGTTGCCTTG | 4204966 | TAAGAAAAG | 4204995 | AGTTGTGTAAGAAAAGC | 4205024 | 3 | 352518-A |
| 20 | ATCAGAGGGTG | 4204967 | GGTGCTAA | 4204996 | ATTAGGAGAGTGGGTGCTAAGT | 4205025 | 3 | 352511-A |
| 21 | ATGGTGGGAG | 4204968 | AGTTGTCAGT | 4204997 | TGGAGGAGAGTTGTCAGTATAG | 4205026 | 3 | 353484-A |
| 22 | CCCAGGAAG | 4204969 | TGGAGCCTGGC | 4204998 | CCCGGGTGGAGCCTGGCTGTG | 4205027 | 3 | 351990-A |
| 23 | GGGCAGTGG | 4204970 | GGTCGGT | 4204999 | AGGGCAGGAGGTCCGTCCCTTC | 4205028 | 3 | 353880-A |
| 24 | GGGCAGTGG | 4204971 | TCTAGAC | 4205000 | GTGACAGTGAATCTAGACAGAC | 4205029 | 3 | 352810-A |
| 25 | TCAAGCTCATTC | 4204972 | CACTAAA | 4205001 | CTCAGCTCATCCACTAAATCCC | 4205030 | 3 | 353184-A |
| 26 | TGGAAAGTT | 4204973 | GGTTGTATGGTT | 4205002 | GGAATGGTGGTTGTATGGTTG | 4205031 | 3 | 353855-A |
| 27 | TGGAGAGTT | 4204974 | CCATATTTG | 4205003 | TGATAGATCCATATTTGGTAA | 4205032 | 3 | 352004-A |
| 28 | TGGAGAGTT | 4204975 | GTTTGTACAGT | 4205004 | TGGGTTTGTGTTGTACAGTGT | 4205033 | 3 | 353160-A |
| 29 | TCACTGCAAC | 4204976 | CTCCACC | 4205005 | TCACTGCAACCTCCACCTCCG | 4205034 | 0 | 353856-A |

REPLACEMENT SHEET

FIG. 21B

| R O W | PRIMER SEQUENCE | SEQ ID NO | SEQUENCED PRIMER | SEQ ID NO | GAM RNA SEQUENCE | SEQ ID NO | GAM PRECURSOR | | | | START OFFSET |
|-------------|--------------------|--------------|--------------------------|--------------|---------------------------|--------------|---|--------------|-------------|----------------------------|--------------|
| | | | | | | | SEQUENCE | SEQ ID NO | C H R | S T R A N D | |
| 1 | GGAAAGAAT | 4205051 | GGAAAGAATG TGGTGCA | 4205059 | GGAAAGGAAA GTGGGTGCAC | 4205067 | GACAGTGGCAATGGGGAAAGGAAAGTGG GTGCACTCAAGCTGGCAGAACGCTAG GCAAGATGTGTAACTGGTTCAACTCTGC ATAGAGGAGAATGTAGGTCTTCCATTCT AATATAGATGTC | 4205075 | 11 | + | 6527398 |
| 2 | GCAAGCGCG | 4205052 | GCAAGAGGCG AGAACGAGA | 4205060 | GCAAGAGTGA GAAGCAGA | 4205068 | CCCAGGTTCTGCAAGAGTGAGAAGCAGAA AGCCTACTTTGCGTTGCCTCTACCTGAGGA GAAGAACGCCAGGTGTGCTCTCAGATGTC GGGGTAGTGCTTGGG | 4205076 | 20 | + | 10164522 |
| 3 | GGAAAGAAT | 4205053 | GGAAAGAATT AATGTGAG | 4205061 | GGAAAGGATA ATGTGAG | 4205069 | ATTCCTCATGTTGGCTAAAGAGACTCCA ACTGCTTGGCCTTTCTGAACCTACTATT AAGAGGAAAGGATAATGTAGGCAGGCTA GTATGGACCTGTTACTCCGATTTCATCAA ATGGAGCTT | 4205077 | 21 | + | 24398831 |
| 4 | GGAAAGAAT | 4205054 | GGAAAGAATT AATGTGAA | 4205062 | GGAAAGATAA TGTGAA | 4205070 | GCTAGAGAGTTGAGACCGAGTGAAGGCCA CACCTCCGGAGGGAAAGATAATGTGAAGG CTCTCTCCACTGACATGTCACATGCTTCT ACTTGACTGGGCTTCCCTAAACTGGGTAA TTTCAGC | 4205078 | 6 | + | 50974009 |
| 5 | CTTTTGCCCTG | 4205055 | CTTTTGCCCTG GGCAGGGC | 4205063 | CTTTTGCAAG GCAGGGC | 4205071 | CTCTTCTAACTTCAGTCCTTTGCAGGGC AGGGCTTACTCTAGGAAACTTATTGCAAG GTAAGTCAAGTCCTAACGGTCTGGCCACT CAGAG | 4205079 | 5 | - | 65170275 |
| 6 | CTCTCTGGT | 4205056 | CTCTCTGGTT AGTACTTGGA | 4205064 | CTAGTCTGGTT AGTACTTGGA | 4205072 | AGGGTCTAGTCGGTTAGTACTGGATGA GAGAGACCAAATAGCAAATACTTAAATG TCTTTCTAACGGAAATTAAATTGGCTCCT | 4205080 | 11 | + | 88695685 |
| 7 | GCAAGAGGCG | 4205057 | GCAAGAGGCG AGAACGAGT | 4205065 | GCAGAGGCAG AAGCAGT | 4205073 | TCTTGCCCTGCAGTCCTAAATCTGCC TGGCTTCTGCCTGACTGCACACTAAGAAT CATGCACAGAACGAGGGCAGAACGAG TGATTGGTAAGG | 4205081 | 1 | + | 193722202 |
| 8 | CTCTCTGGTTA | 4205058 | CTCTCTGGTT AGTAAATAGG | 4205066 | CTCTCTGGAGA GTAATAGG | 4205074 | CTTGAGAAAAAGAGGCTTGTATATTCC AAGCATGAGATGATTATTAGAACACTTA TTTCTGTTCTCTGGAGAGTAATAGGCA TAACCCCTTATCAGGG | 4205082 | 2 | - | 240247210 |